

GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: November 2, 2005, 10:55:28 / Search time 43 Seconds

(Without alignment)

612.817 Million cell updates/sec

Title: US-09-905-075-2

Perfect score: 2005

Sequence: 1 MRLPRALGILLPLLLPLP.....ABARTRGSPPTQPSRDL 353

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Maximum Match 100%

Maximum Match 100%

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Maximum Match 100%

Maximum Match 100%

Maximum Match 100%

Maximum Match 100%

BEST AVAILABLE COPY

101	222	11.1	2556	4	US-08-899-232-2	Sequence 2, Appl1	174	203	10.1	443	3	US-08-980-514-1	Sequence 1, Appl1
102	222	11.1	2556	4	US-09-121-457-2	Sequence 2, Appl1	175	203	10.1	717	3	US-08-872-855-9	Sequence 1, Appl1
103	221	11.0	1446	4	US-09-919-497-85	Sequence 85, Appl1	176	202.5	10.1	384	4	US-09-312-283C-389	Sequence 189, App
104	221	11.0	1447	4	US-09-961-403-14	Sequence 7, Appl1	177	201	10.0	383	4	US-08-597-545-2	Sequence 2, Appl1
105	220.5	11.0	1010	4	US-08-882-046-7	Sequence 7, Appl1	178	201	10.0	383	4	US-08-457-335-2	Sequence 2, Appl1
106	220.5	11.0	1010	4	US-09-028-740A-6	Sequence 7, Appl1	179	201	10.0	387	3	US-08-457-335-2	Sequence 2, Appl1
107	220.5	11.0	1033	4	US-09-028-740A-6	Sequence 18, Appl1	180	201	10.0	387	3	US-08-831-943C-9	Sequence 9, Appl1
108	220.5	11.0	1067	4	US-09-579-535C-18	Sequence 7, Appl1	181	201	10.0	387	3	US-08-980-514-3	Sequence 5, Appl1
109	220.5	11.0	1187	4	US-09-068-740A-7	Sequence 7, Appl1	182	201	10.0	387	3	US-09-212-168-5	Sequence 3, Appl1
110	220.5	11.0	1208	4	US-09-199-865-1	Sequence 1, Appl1	183	201	10.0	387	4	US-09-409-096-2	Sequence 2, Appl1
111	220.5	11.0	1308	4	US-10-113-329-1	Sequence 1, Appl1	184	201	10.0	387	4	US-09-322-357-1	Sequence 1, Appl1
112	220.5	11.0	1318	4	US-08-400-159-6	Sequence 6, Appl1	185	201	10.0	823	4	US-09-949-016-6852	Sequence 6852, Ap
113	220.5	11.0	1318	4	US-08-611-729A-6	Sequence 6, Appl1	186	201	10.0	823	4	US-09-631-603-9	Sequence 9, Appl1
114	220.5	11.0	1318	4	US-08-882-046-2	Sequence 2, Appl1	187	200.5	10.0	943	3	US-08-476-515A-12	Sequence 12, Appl1
115	220.5	11.0	1318	4	US-09-114-776-7	Sequence 7, Appl1	188	200.5	10.0	944	3	US-08-652-877-12	Sequence 12, Appl1
116	220.5	11.0	1318	4	US-09-068-740A-11	Sequence 7, Appl1	189	200.5	10.0	4654	3	US-08-476-515A-84	Sequence 84, Appl1
117	220.5	11.0	1318	4	US-09-855-122-7	Sequence 7, Appl1	190	200.5	10.0	4654	3	US-08-652-877-84	Sequence 84, Appl1
118	220.5	11.0	1318	4	US-09-855-122-7	Sequence 8, Appl1	191	200.5	10.0	4652	3	US-08-652-877-84	Sequence 84, Appl1
119	220.5	11.0	1318	4	US-09-855-122-7	Sequence 8, Appl1	192	200.5	10.0	4652	3	US-08-652-877-88	Sequence 88, Appl1
120	220.5	11.0	1318	4	US-09-195-524-6	Sequence 8, Appl1	193	200.5	10.0	4655	3	US-08-652-877-90	Sequence 90, Appl1
121	220.5	11.0	1318	4	US-09-579-535C-1	Sequence 1, Appl1	194	199	9.9	578	3	US-08-628-747-2	Sequence 2, Appl1
122	220.5	11.0	1318	4	US-09-949-016-5902	Sequence 5902, Ap	195	199	9.9	578	3	US-08-981-392-13	Sequence 13, Appl1
123	220.5	11.0	1254	4	US-09-949-016-5902	Sequence 10297, Ap	196	198	9.9	578	3	US-09-908-322-13	Sequence 13, Appl1
124	220.5	11.0	1254	4	US-09-949-016-5902	Sequence 10297, Ap	197	198	9.9	578	3	US-08-872-855-7	Sequence 7, Appl1
125	220	11.0	466	4	US-09-949-016-7792	Sequence 7792, Ap	198	198	9.9	721	3	US-08-981-392-5	Sequence 5, Appl1
126	218.5	10.9	675	6	5258288-1	Patent No. 5258288	199	198	9.9	721	3	US-08-981-392-5	Sequence 5, Appl1
127	218.5	10.9	675	6	5258288-1	Patent No. 5258288	200	198	9.9	721	4	US-09-949-016-10381	Sequence 10381, A
128	216.5	10.8	2703	4	US-08-185-432-19	Sequence 19, Appl1	201	198	9.9	846	4	US-08-982-045-4	Sequence 4, Appl1
129	216.5	10.8	2703	4	US-08-899-232-4	Sequence 4, Appl1	202	197.5	9.9	1148	3	US-08-982-045-4	Sequence 4, Appl1
130	216.5	10.8	2703	4	US-08-899-232-4	Sequence 4, Appl1	203	197.5	9.9	1148	3	US-08-982-045-4	Sequence 4, Appl1
131	215.5	10.7	2471	4	US-08-125-432-16	Sequence 16, Appl1	204	197	9.8	520	3	US-09-068-740A-3	Sequence 3, Appl1
132	215.5	10.7	2471	4	US-08-083-590A-19	Sequence 19, Appl1	205	197	9.8	702	3	US-09-068-740A-4	Sequence 4, Appl1
133	215.5	10.7	2471	4	US-08-533-384-19	Sequence 19, Appl1	206	197	9.8	723	3	US-09-068-740A-9	Sequence 9, Appl1
134	215.5	10.7	2471	4	US-08-899-232-1	Sequence 1, Appl1	207	197	9.8	723	4	US-09-423-753-27	Sequence 27, Appl1
135	215.5	10.7	2471	4	US-09-121-457-1	Sequence 1, Appl1	208	197	9.8	816	2	US-08-820-1170A-37	Sequence 37, Appl1
136	214	10.7	2321	4	US-09-230-652-2	Sequence 2, Appl1	209	196.5	9.8	816	3	US-09-055-693-17	Sequence 17, Appl1
137	213	10.6	673	3	US-08-282-141-3	Sequence 1, Appl1	210	196.5	9.8	816	3	US-09-273-565-37	Sequence 37, Appl1
138	213	10.6	673	3	US-08-435-351-1	Sequence 1, Appl1	211	196.5	9.8	816	3	US-09-565-538-17	Sequence 17, Appl1
139	213	10.6	673	3	US-08-438-863-1	Sequence 1, Appl1	212	196.5	9.8	816	3	US-09-565-538-17	Sequence 17, Appl1
140	213	10.6	673	3	US-08-438-863-1	Sequence 1, Appl1	213	196.5	9.8	816	3	US-09-565-538-17	Sequence 17, Appl1
141	213	10.6	673	3	US-08-438-863-1	Sequence 1, Appl1	214	196	9.8	678	1	US-08-438-863-2	Sequence 2, Appl1
142	213	10.6	673	3	US-08-438-863-1	Sequence 1, Appl1	215	196	9.8	678	1	US-08-438-863-2	Sequence 2, Appl1
143	213	10.6	673	3	US-08-438-863-1	Sequence 1, Appl1	216	196	9.8	678	1	US-08-438-863-2	Sequence 2, Appl1
144	213	10.6	673	3	US-08-438-863-1	Sequence 1, Appl1	217	196	9.8	678	1	US-08-438-863-2	Sequence 2, Appl1
145	212	10.6	383	4	US-09-142-027A-12	Sequence 12, Appl1	218	196	9.8	678	2	US-08-438-863-2	Sequence 2, Appl1
146	211.5	10.5	810	2	US-08-820-170A-34	Sequence 34, Appl1	219	196	9.8	678	2	US-08-438-863-2	Sequence 2, Appl1
147	211.5	10.5	810	2	US-09-055-693-34	Sequence 34, Appl1	220	196	9.8	678	3	US-08-438-863-2	Sequence 2, Appl1
148	211.5	10.5	810	2	US-09-273-565-34	Sequence 34, Appl1	221	196	9.8	678	3	US-08-438-863-2	Sequence 2, Appl1
149	211.5	10.5	810	2	US-09-565-538-34	Sequence 34, Appl1	222	196	9.8	678	3	US-08-438-863-2	Sequence 2, Appl1
150	211.5	10.5	810	2	US-09-661-468-14	Sequence 14, Appl1	223	196	9.8	713	3	US-08-872-855-5	Sequence 5, Appl1
151	211.5	10.5	810	2	US-09-661-468-14	Sequence 14, Appl1	224	196	9.8	713	3	US-08-872-855-5	Sequence 5, Appl1
152	211.5	10.5	810	2	US-09-661-468-14	Sequence 14, Appl1	225	196	9.8	713	3	US-08-872-855-5	Sequence 5, Appl1
153	211.5	10.5	810	2	US-09-661-468-14	Sequence 14, Appl1	226	196	9.8	713	3	US-08-872-855-5	Sequence 5, Appl1
154	209.5	10.4	448	4	US-09-231-168-1	Sequence 1, Appl1	227	195.5	9.8	685	4	US-08-872-855-2	Sequence 2, Appl1
155	209.5	10.4	448	4	US-09-231-168-1	Sequence 1, Appl1	228	195.5	9.8	685	4	US-08-872-855-2	Sequence 2, Appl1
156	209.5	10.4	448	4	US-09-231-168-1	Sequence 1, Appl1	229	195.5	9.8	685	4	US-08-872-855-2	Sequence 2, Appl1
157	208.5	10.4	448	4	US-09-409-096-4	Sequence 4, Appl1	230	195	9.7	830	3	US-09-641-612-7	Sequence 7, Appl1
158	208.5	10.4	448	4	US-09-214-776-2	Sequence 2, Appl1	231	194	9.6	729	3	US-08-872-855-11	Sequence 11, Appl1
159	208.5	10.4	1055	4	US-09-855-723-2	Sequence 2, Appl1	232	193	9.6	720	3	US-08-872-855-8	Sequence 8, Appl1
160	207	10.3	1065	2	US-08-400-159-8	Sequence 8, Appl1	233	193	9.6	722	3	US-08-981-392-12	Sequence 12, Appl1
161	207	10.3	1112	4	US-09-214-776-3	Sequence 3, Appl1	234	193	9.6	722	4	US-09-908-322-5	Sequence 5, Appl1
162	207	10.3	1112	4	US-09-855-122-3	Sequence 3, Appl1	235	192.5	9.6	728	3	US-08-981-392-2	Sequence 2, Appl1
163	207	10.3	1112	4	US-09-214-776-5	Sequence 5, Appl1	236	192.5	9.6	728	3	US-08-981-392-2	Sequence 2, Appl1
164	207	10.3	1112	4	US-09-214-776-5	Sequence 5, Appl1	237	192.5	9.6	728	3	US-08-981-392-2	Sequence 2, Appl1
165	207	10.3	1112	4	US-09-214-776-5	Sequence 5, Appl1	238	192.5	9.6	728	3	US-08-981-392-2	Sequence 2, Appl1
166	206.5	10.3	1193	2	US-09-186-930-186	Sequence 186, App	239	192.5	9.6	833	1	US-08-083-590A-2	Sequence 2, Appl1
167	206	10.3	1193	2	US-08-400-159-10	Sequence 10, Appl1	240	192.5	9.6	833	1	US-08-465-500-6	Sequence 6, Appl1
168	206	10.3	1193	2	US-08-611-729A-10	Sequence 10, Appl1	241	192.5	9.6	833	2	US-08-346-126-6	Sequence 6, Appl1
169	204	10.2	835	3	US-09-195-524-10	Sequence 10, Appl1	242	192.5	9.6	833	2	US-08-346-126-6	Sequence 6, Appl1
170	204	10.2	835	3	US-09-284-819-6	Sequence 6, Appl1	243	192.5	9.6	833	3	US-08-532-384-2	Sequence 2, Appl1
171	205	10.1	1964	4	US-09-467-597-1	Sequence 12, Appl1	244	193.5	9.6	833	3	US-08-893-826-6	Sequence 6, Appl1
172	205	10.1	1964	4	US-09-467-597-1	Sequence 12, Appl1	245	193.5	9.6	833	3	US-08-893-826-6	Sequence 6, Appl1
173	203	10.1	443	2	US-08-831-963C-2	Sequence 2, Appl1	246	191	9.5	553	3	US-09-249-697A-6	Sequence 6, Appl1

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OW protein - protein search, using BLAST model 167 Seconds  
Run on: November 2, 2005, 10:11:35 (without alignment)  
817.523 Million cell updates/sec

Title: US-09-905-075-2

Perfect score: 2005

Sequence: 1 MRLPRAALGLPLLLLLP.....AEKATGSPQLPERDL 353

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
2105692 seqs, 36676081 residues

Searched: Minimum number of hits satisfying chosen parameters: 2105692

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100

Database: 1. Geneseq 156Dec04

2. Geneseq 1998Dec04

3. Geneseq 2000Dec04

4. Geneseq 2001Dec04

5. Geneseq 2002Dec04

6. Geneseq 2003Dec04

7. Geneseq 2004Dec04

8. Geneseq 2005Dec04

Pred. No. 10 the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the score distribution.

Result 1 Score Match Length DB ID Description

ID AAV05283 standard; protein; 353 AA.

DE EGF-like homologue PRO211.

PN MO9914327-A2.

PD 25-MAR-1999.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 2 Score Match Length DB ID Description

ID AAV09064 standard; protein; 353 AA.

DE Human EGF-like homologue protein (PRO217) encoded by DNA32292 cDNA.

PN MO9914421-A2.

PD 25-MAR-1999.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 3 Score Match Length DB ID Description

ID AAV13344 standard; protein; 353 AA.

DE Amino acid sequence of protein PRO211.

PN MO9914428-A2.

PD 25-MAR-1999.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 4 Score Match Length DB ID Description

ID AAV83224 standard; protein; 353 AA.

DE PRO211 Polypeptide.

PN MO300021996-A2.

PD 20-APR-2000.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 3; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 5 Score Match Length DB ID Description

ID AAV130169 standard; protein; 353 AA.

DE PRO211 Polypeptide.

PN MO300005319-A1.

PD 21-SEP-2000.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 3; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 6 Score Match Length DB ID Description

ID ADC78322 standard; protein; 353 AA.

DE Human PRO211 protein.

PN MO200015766-A2.

PD 25-JAN-2001.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 3; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 7 Score Match Length DB ID Description

ID AAB80212 standard; protein; 353 AA.

DE Human PRO211 protein.

PN MO200104311-A1.

PD 18-JAN-2001.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 4; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 8 Score Match Length DB ID Description

ID AAB61231 standard; protein; 353 AA.

DE Human TM60 331 protein.

PN MO200106638-A2.

PD 04-JAN-2001.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 2005; DB 4; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 9 Score Match Length DB ID Description

ID AAV12319 standard; protein; 353 AA.

DE Human PRO211 polypeptide sequence.

PN MO200140466-A2.

PD 07-JUN-2001.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 4; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 10 Score Match Length DB ID Description

ID AAB53075 standard; protein; 353 AA.

DE Human angiogenesis-associated protein PRO211, SEQ ID NO:57.

PN MO2000053753-A2.

PD 14-SEP-2000.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 4; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 11 Score Match Length DB ID Description

ID AAB58596 standard; protein; 353 AA.

DE PRO211

PN MO200105836-A1.

PD 25-JAN-2001.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 4; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 12 Score Match Length DB ID Description

ID AABU71590 standard; protein; 353 AA.

DE Human PRO polypeptide #1.

PN US2002146709-A1.

PD 10-OCT-2002.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 6; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 13 Score Match Length DB ID Description

ID ABO17763 standard; protein; 353 AA.

DE Novel human secreted and transmembrane protein PRO211.

PN US2003032156-A1.

PD 13-FEB-2003.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 6; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 14 Score Match Length DB ID Description

ID AABU71445 standard; protein; 353 AA.

DE Human PRO polypeptide #1.

PN US2002182659-A1.

PD 19-DEC-2002.

PA (GRTN) GENENTECH INC.

Query Match 100.0%; Score 2005; DB 6; Length 353;

Best Local Similarity 100.0%; Pred. No. 6e-131;

Result 15 Score Match Length DB ID Description

ID AABU81017 standard; protein; 353 AA.

DE Human PRO polypeptide #148.

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OM protein - protein search, using sw model

Run on: November 2, 2005, 10:42:37 ; Search time 176 Seconds

(Without alignment)  
1027.068 Million cell updates/sec

Title: US-09-905-075-2

Perfect score: 2005  
Sequence: 1 MRLRRALGLPLLLALLPP.....AEAEATGSGPTQLPSRDL 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 01  
Maximum Match 1001  
Length filter 1500 summaries

Database: UniProt 03.  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match Length	ID	Description
1	205	100.0	06XU1	06xui1 homo sapien
2	195	99.5	06XU0	06xui0 homo sapien
3	179	89.1	06BU47	06bu47 homo sapien
4	153.5	76.5	06CY40	06cy40 mus musculu
5	148.5	73.9	06CY48	06cy48 mus musculu
6	1020.5	50.9	07SKF6	07skf6 brachydanio
7	971.5	48.5	07SKF6	07skf6 mus sapien
8	969	48.3	06NHD1	06nhd1 homo sapien
9	968.5	48.3	06NHD1	06nhd1 mus musculu
10	959.5	47.9	07XAD7	07xad7 homo sapien
11	959.5	47.9	07XAD7	07xad7 mus musculu
12	689	34.9	06S584	06s584 mus sapien
13	670	33.4	06VJ20	06vj20 drosophila
14	655.5	32.7	07OJ30	07oj30 anopheles g
15	599.5	29.9	06DPE9	06dpe9 oncorhynch
16	540	26.9	06DPE9	06dpe9 mus musculu
17	423	21.1	06BY28	06by28 mus musculu
18	286.5	14.3	06BY28	06by28 mus musculu
19	279.5	13.9	06BY28	06by28 mus musculu
20	279	13.9	06BY28	06by28 mus musculu
21	277.5	13.8	06BY28	06by28 mus musculu
22	274.5	13.6	06BY28	06by28 mus musculu
23	274.5	13.7	06BY28	06by28 mus musculu
24	272	13.6	06BY28	06by28 mus musculu
25	271.5	13.5	06BY28	06by28 mus musculu
26	271.5	13.5	06BY28	06by28 mus musculu
27	271	13.5	06BY28	06by28 mus musculu
28	270.5	13.5	06BY28	06by28 mus musculu
29	268.5	13.4	06BY28	06by28 mus musculu
30	268.5	13.4	06BY28	06by28 mus musculu
31	268.5	13.4	06BY28	06by28 mus musculu

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105	236	11.8	961	2	09E0C6	09e0c6 mus musculus	178	218.5	10.9	2516	2	07T052	07t052 mus musculus
106	236	11.8	1972	2	08WPL1	08wpl1 olkopleura	179	218.5	10.9	2526	2	07T051	07t051 mus musculus
107	236	11.8	2524	2	09GPAS	09gpas brachiolepto	180	218.5	10.9	2531	2	08K428	08k428 mus musculus
108	235.5	11.7	576	2	09YJVT	09yjt7 homo sapien	181	218.5	10.9	2531	2	07T050	07t050 mus musculus
109	235.5	11.7	1222	2	07PPC0	07ppc0 anophelies g	182	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
110	234	11.7	1056	2	07494	07494 caenothabdi	183	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
111	233	11.6	992	2	08E029	08e029 homo sapien	184	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
112	233	11.6	992	2	08E029	08e029 homo sapien	185	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
113	233	11.6	992	2	08E029	08e029 homo sapien	186	218	10.9	2471	1	NTC1_PAT	NTC1_PAT
114	232	11.6	969	2	08IYV8	08iyv8 homo sapien	187	217.5	10.8	1242	1	060784	060784 mus musculus
115	232	11.6	1375	1	NTD1_HUMAN	014112 homo sapien	188	217.5	10.8	1242	1	JMGI_BRARE	JMGI_BRARE
116	232	11.6	1398	2	08APM6	08apm6 xenopus lae	189	217.5	10.8	3704	2	08BTV4	08bTV4 mus musculus
117	231.5	11.5	827	2	06BPC9	06bpc9 mus musculus	190	217	10.7	545	2	09J025	09j025 mus musculus
118	231.5	11.5	862	2	09UP98	09up98 homo sapien	191	216.5	10.8	327	2	08BPM6	08bpm6 mus musculus
119	231.5	11.5	993	2	06PEY1	06pey1 mus musculus	192	216.5	10.8	550	2	09J025	09j025 mus musculus
120	231	11.5	500	2	0864U4	0864u4 bos taurus	193	216.5	10.8	2673	1	0966C3	0966C3 mus musculus
121	231	11.5	578	2	0912D3	0912d3 mus musculus	194	216.5	10.8	2673	1	0966C3	0966C3 mus musculus
122	230.5	11.5	1399	2	08U130	08u130 xenopus lae	195	216	10.8	579	1	NTC1_PAT	NTC1_PAT
123	230.5	11.5	1399	2	08U130	08u130 xenopus lae	196	216	10.8	579	1	NTC1_PAT	NTC1_PAT
124	229.5	11.4	880	2	08NNU9	08nnu9 homo sapien	197	215.5	10.7	609	2	092376	092376 mus musculus
125	229.5	11.4	880	2	08NNU9	08nnu9 homo sapien	198	215.5	10.7	609	2	092376	092376 mus musculus
126	229.5	11.4	880	2	08NNU9	08nnu9 homo sapien	199	215.5	10.7	609	2	092376	092376 mus musculus
127	229.5	11.4	880	2	08NNU9	08nnu9 homo sapien	200	215	10.7	2471	1	NTC1_HUMAN	NTC1_HUMAN
128	229	11.4	674	2	07OWP1	07owp2 penaeus jap	201	215	10.7	823	2	07P6Q4	07p6Q4 mus musculus
129	228.5	11.4	649	1	PTES_MACHU	07w612 giardia lam	202	214.5	10.7	1246	1	BPJ3_HUMAN	BPJ3_HUMAN
130	228.5	11.4	886	1	EMR1_HUMAN	028530 maceca mla	203	214.5	10.7	448	1	FBLS_MOUSE	FBLS_MOUSE
131	228.5	11.4	1213	1	JNG1_BRARE	090Y54 brachydanio	204	214.5	10.7	724	2	07OTU1	07otU1 mus musculus
132	228	11.4	1218	1	JNG1_BRARE	090Y54 mus musculus	205	214	10.7	827	1	NTC1_HUMAN	NTC1_HUMAN
133	228	11.4	1218	1	JNG1_BRARE	090Y54 mus musculus	206	213.5	10.6	978	2	08E0T3	08e0T3 mus musculus
134	226.5	11.3	1679	1	PMR2_MOUSE	P10432 dirosophila	207	213.5	10.6	978	2	08E0T3	08e0T3 mus musculus
135	226.5	11.3	1679	1	PMR2_MOUSE	08e0T3 mus musculus	208	213.5	10.6	978	2	08E0T3	08e0T3 mus musculus
136	226.5	11.3	1679	1	PMR2_MOUSE	08e0T3 mus musculus	209	213.5	10.6	978	2	08E0T3	08e0T3 mus musculus
137	226	11.3	592	2	091XLS	091x15 gallus galli	210	213	10.6	674	2	GA66_MOUSE	GA66_MOUSE
138	226	11.3	592	2	091XLS	091x15 mus musculus	211	212.5	10.6	569	2	07OXT3	07OXT3 mus musculus
139	225.5	11.2	2531	1	PTES_FABIT	090Y42 xenopus lae	212	212.5	10.6	911	2	068XFA	068XFA mus musculus
140	225.5	11.2	1214	2	09OYD2	090Y42 xenopus lae	213	212.5	10.6	1245	2	06PBM3	06pBM3 mus musculus
141	225	11.2	650	2	Q16519	Q16519 homo sapien	214	212.5	10.6	1335	2	07R1M3	07r1M3 mus musculus
142	225	11.2	1018	2	06NZL6	06nz18 mus musculus	215	212	10.6	719	2	09J021	09j021 mus musculus
143	224.5	11.2	608	2	080V54	080V54 mus musculus	216	212	10.6	218	1	NTC1_MOUSE	NTC1_MOUSE
144	224.5	11.2	1394	2	08CE22	08CE22 mus musculus	217	211.5	10.5	396	2	08L0D0	08L0D0 mus musculus
145	224.5	11.2	1403	2	NTD2_MOUSE	08CE22 mus musculus	218	211.5	10.5	396	2	08L0D0	08L0D0 mus musculus
146	224.5	11.2	1403	2	NTD2_MOUSE	08CE22 mus musculus	219	211.5	10.5	396	2	08L0D0	08L0D0 mus musculus
147	224.5	11.2	1403	2	NTD2_MOUSE	08CE22 mus musculus	220	211.5	10.5	810	2	06N5T4	06N5T4 mus musculus
148	224.5	11.2	1403	2	NTD2_MOUSE	08CE22 mus musculus	221	211.5	10.5	931	1	EMR1_MOUSE	EMR1_MOUSE
149	224.5	11.2	1574	2	BPJ3_PAT	088281 ratius norv	222	221	10.5	2437	1	NTC1_BRARE	NTC1_BRARE
150	224.5	11.2	2447	2	013149	013149 fugu rubrip	223	221	10.5	764	2	07OZT9	07OZT9 mus musculus
151	224	11.2	1219	1	JNG1_PAT	063722 ratius norv	224	224	11.1	1577	2	09B8V9	09B8V9 mus musculus
152	223	11.1	650	2	Q9NSD0	Q9NSD0 homo sapien	225	225	10.5	5636	2	068W67	068W67 mus musculus
153	223	11.1	1519	1	Q9NSD0	Q9NSD0 homo sapien	226	226	10.5	185	2	06X1W9	06x1W9 mus musculus
154	223	11.1	2524	2	NOTC1_XENLA	P21783 xenopus lae	227	210.5	10.5	517	2	09N701	09N701 mus musculus
155	223	11.1	535	2	07OQZ3	07OQZ3 anophelies g	228	210	10.5	278	1	NTC1_BRARE	NTC1_BRARE
156	222.5	11.1	1441	2	07E0X9	07E0X9 homo sapien	229	210	10.5	278	1	NTC1_BRARE	NTC1_BRARE
157	222.5	11.1	1441	2	07E0X9	07E0X9 homo sapien	230	210	10.5	278	1	NTC1_BRARE	NTC1_BRARE
158	222.5	11.1	1441	2	07E0X9	07E0X9 homo sapien	231	210	10.5	674	2	07O8Z7	07O8Z7 mus musculus
159	222.5	11.1	4007	1	PRB1_HUMAN	086x38 homo sapien	232	210	10.5	2428	2	0816X6	0816X6 mus musculus
160	222	11.1	347	2	Q9DDR4	09ddr4 gallus galli	233	209.5	10.4	448	1	FBLS_HUMAN	FBLS_HUMAN
161	222	11.1	675	1	PTES_BOVIN	P07224 bog taurus	234	209.5	10.4	609	2	07QNX8	07QNX8 mus musculus
162	222	11.1	838	2	018761	018761 caenothabdi	235	209.5	10.4	626	2	08ND91	08ND91 mus musculus
163	222	11.1	1212	1	LTB1_PAT	Q27422 caenothabdi	236	209.5	10.4	687	1	VS41_GIALA	VS41_GIALA
164	222	11.1	1212	1	LTB1_PAT	Q27422 caenothabdi	237	209.5	10.4	687	1	VS41_GIALA	VS41_GIALA
165	222	11.1	2556	1	NTC1_HUMAN	Q00918 ratius norv	238	209.5	10.4	1615	2	096KQ6	096KQ6 mus musculus
166	221	11.0	1247	1	NTD1_MOUSE	P14531 homo sapien	239	209	10.4	715	2	07OZU9	07OZU9 mus musculus
167	221	11.0	2470	1	NTC1_MOUSE	P14531 homo sapien	240	209	10.4	715	2	07OZU9	07OZU9 mus musculus
168	220.5	11.0	1247	1	NTC1_MOUSE	P14531 homo sapien	241	209	10.4	715	2	07OZU9	07OZU9 mus musculus
169	220.5	11.0	1247	1	NTC1_MOUSE	P14531 homo sapien	242	209	10.4	715	2	07OZU9	07OZU9 mus musculus
170	220.5	11.0	1247	1	NTC1_MOUSE	P14531 homo sapien	243	209	10.4	715	2	07OZU9	07OZU9 mus musculus
171	220	11.0	739	2	08AV18	08av18 rana esculle	244	208.5	10.4	642	2	08P3V5	08P3V5 mus musculus
172	220	11.0	913	2	08AV18	08av18 rana esculle	245	208.5	10.4	642	2	08P3V5	08P3V5 mus musculus
173	220	11.0	1062	2	060789	060789 mus musculus	246	208	10.4	443	1	FBJ4_CRIGR	FBJ4_CRIGR
174	220	11.0	2531	1	NTC1_PAT	Q07008 ratius norv	247	207	10.3	709	2	09XJ37	09XJ37 mus musculus
175	220	11.0	3623	2	Q70244	Q70244 ratius norv	248	207	10.3	443	2	09J006	09J006 mus musculus
176	218.5	10.9	461	2	P97883	P97883 ratius norv	249	207	10.3	648	2	Q29094	Q29094 mus musculus
177	218.5	10.9	1025	2	Q7R6J7	Q7R6J7 giardia lam	250	207	10.3	947	2	Q8BKX7	Q8BKX7 mus musculus

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OM protein - protein search, using sw model

Run on: November 2, 2005, 10:50:59 | Search time 40 seconds

(without alignment) 849.113 Million cell updates/sec

Title: US-09-905-075-2

Portect score: 2005 1 MLPRRAALCLPLLLLP.....AEABATEGSPQLPSHDL 353

Sequence: 1 MLPRRAALCLPLLLLP.....AEABATEGSPQLPSHDL 353

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Database: 1. p1r.79.1  
2. p1r.1.1  
3. p1r.1.1  
4. p1r.1.1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	959.5	47.9	417	2	T08724	hypothetical prote
2	940	26.9	366	2	T20656	hypothetical prote
3	770	13.5	2871	2	A55567	fibulin-1 - bovi
4	268.5	13.4	3002	2	A47221	fibulin-1 precu
5	268	13.4	1548	2	A55493	latent transform
6	263	13.1	1548	2	G14583	serine proteinase
7	254.5	12.7	683	2	B34536	fibulin-1 precu
8	254.5	12.7	683	2	G14536	fibulin-1 precu
9	253.5	12.6	705	2	G14568	fibulin-1 precu
10	253.5	12.6	3507	2	T14513	hypothetical prote
11	252.5	12.6	2871	2	A55624	fibulin-1 precu
12	252.5	12.6	2871	2	A55624	fibulin-1 precu
13	250	12.5	3623	2	T09456	intrinsic factor-B
14	249.5	12.4	2918	2	A54105	fibulin-2 precu
15	248	12.4	915	1	A46225	subtilisin-like pr
16	247	12.3	675	1	KX875	plasma protein S p
17	247	12.3	1221	2	A49457	fibulin-2 precu
18	246.5	12.3	1221	2	A57253	latent transform
19	246.5	12.3	1221	2	A57253	latent transform
20	245.5	12.2	1384	2	A16626	hypothetical prote
21	245.5	12.2	1384	2	A16626	hypothetical prote
22	240.5	12.0	1394	2	A16626	transforming grow
23	239	11.9	915	1	KX875	plasma protein S p
24	239	11.9	915	1	KX875	probable protease
25	239	11.9	1299	2	T43251	furin (EC 3.4.21.7
26	236	11.8	899	2	G02428	subtilisin-like pr
27	236	11.8	915	1	JC6148	subtilisin-like pr
28	234	11.7	1106	2	T18739	hypothetical prote
29	232	11.6	675	1	KX875	plasma protein S p

30	232	11.6	1376	2	G00043	osteonidogen - hum
31	231.5	11.5	1069	2	T43601	hypothetical prote
32	228.5	11.4	642	2	S53434	plasma protein S p
33	228	11.4	1680	2	A53434	furin (EC 3.4.21.7
34	227	11.3	2234	2	A53434	notch protein-1
35	226.5	11.2	2234	2	A53434	notch protein-1
36	225.5	11.2	1646	2	S19819	plasma protein S -
37	224.5	11.2	1574	2	T13954	plasma protein S -
38	224	11.2	1220	2	A56136	probable protease
39	222.5	11.1	886	1	A51172	plasma protein S p
40	222	11.1	675	1	KX875	hypothetical prote
41	222	11.1	838	2	T20125	masking protein pr
42	222	11.1	1712	2	A38261	notch B protein -
43	221	11.0	1203	2	A49175	notch B protein -
44	221	11.0	1247	1	MMHUND	notch B protein -
45	221	11.0	2555	2	A40043	notch protein homo
46	220	11.0	2555	2	A40043	notch protein homo
47	220	11.0	2555	2	A40043	notch protein homo
48	218	10.9	2432	2	A49128	cell-fate determin
49	217.5	10.8	1357	2	T16680	hypothetical prote
50	217.5	10.8	3672	2	T23433	hypothetical prote
51	217.5	10.8	3704	2	T73316	probable laminin a
52	216.5	10.8	2703	1	A24420	notch protein - fr
53	216	10.7	2321	2	S78549	notch protein - h
54	213.5	10.6	1245	1	MMMSND	plasma protein S p
55	213	10.6	642	2	S53433	growth arrest-1
56	213	10.6	673	2	A48089	notch 3 protein
57	212	10.6	2338	2	S43306	notch 3 protein
58	211.5	10.5	1430	2	T27283	growth potential
59	211.5	10.5	1430	2	T27283	growth potential
60	210	10.5	674	2	T54476	growth potential
61	209	10.4	1766	2	A42125	growth potential
62	209	10.4	2139	2	A35672	growth potential
63	205.5	10.2	473	2	A56175	adhesive plaque pr
64	204.5	10.2	810	2	T10756	notch homolog - se
65	204.5	10.2	1964	2	T09059	notch homolog - se
66	204	10.2	2531	2	T31070	notch homolog - se
67	203.5	10.1	2352	2	A32021	notch homolog - se
68	202.5	10.1	356	2	A23918	notch homolog - se
69	202.5	10.1	689	2	T42780	notch homolog - se
70	202.5	10.1	689	2	T42780	notch homolog - se
71	202.5	10.1	689	2	T42780	notch homolog - se
72	201	10.0	383	2	S53716	notch homolog - se
73	201	10.0	387	2	T38449	notch homolog - se
74	201	10.0	589	2	T43210	notch homolog - se
75	201	10.0	798	2	T27293	notch homolog - se
76	200.5	10.0	1064	2	A40136	notch homolog - se
77	200	10.0	713	2	A35502	notch homolog - se
78	199.5	10.0	1722	2	B89753	notch homolog - se
79	197.5	9.9	677	2	C42125	notch homolog - se
80	197	9.8	577	2	A65051	notch homolog - se
81	196	9.8	577	2	A65051	notch homolog - se
82	195.5	9.8	688	2	B07520	notch homolog - se
83	195.5	9.8	4135	2	T42629	notch homolog - se
84	195	9.7	493	2	JC5621	notch homolog - se
85	195	9.7	686	2	JC5659	notch homolog - se
86	194.5	9.7	3051	2	S42373	notch homolog - se
87	193	9.6	722	2	T48334	notch homolog - se
88	193	9.6	861	2	A48825	notch homolog - se
89	193	9.6	1274	2	T42017	notch homolog - se
90	192.5	9.6	728	2	T50719	notch homolog - se
91	192.5	9.6	832	2	A12286	notch homolog - se
92	192.5	9.6	832	2	A12286	notch homolog - se
93	192.5	9.6	832	2	A12286	notch homolog - se
94	192.5	9.6	832	2	A12286	notch homolog - se
95	192.5	9.6	832	2	A12286	notch homolog - se
96	191.5	9.6	4006	2	T09070	notch homolog - se
97	191.5	9.6	837	1	A29512	notch homolog - se
98	191	9.5	2823	2	F87968	notch homolog - se
99	191	9.5	2823	2	T23064	notch homolog - se
100	190	9.5	3102	2	T43291	notch homolog - se
101	190	9.5	2406	2	A54148	notch homolog - se
102	189	9.4	575	1	THHND	notch homolog - se

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103	109	9.4	1687	2	T30176	EGF repeat crano
104	108.5	9.4	9922	2	T30176	PACB4 - mouse (fr
105	108.5	9.4	3566	1	A40701	tenascin-X precurs
106	108	9.4	9959	1	A39450	tenascin-X-like pr
107	108	9.4	1111	2	T65972	hypothetical prote
108	108	9.4	1111	2	T65972	hypothetical prote
109	108	9.4	4543	1	A53132	hypothetical prote
110	108	9.4	741	2	T46488	hypothetical prote
111	107.5	9.4	937	2	T53282	gene PACB3 protein
112	107	9.3	385	2	T53718	hypothetical prote
113	107	9.3	385	2	T53718	hypothetical prote
114	106	9.3	621	2	T18467	low density lipopr
115	105.5	9.3	511	2	T17298	hypothetical prote
116	105	9.2	1207	1	EGHU	epidermal growth f
117	105	9.2	1650	2	T53457	dominant autointg
118	105	9.2	1830	2	A12230	tenascin precursor
119	105	9.2	1830	2	A12230	tenascin precursor
120	104.5	9.2	1630	1	MMRP2	gp330 protein prec
121	103.5	9.2	558	2	T17124	hypothetical prote
122	103.5	9.2	1531	2	T42218	hypothetical prote
123	103	9.1	1295	2	A32901	glp1 protein precu
124	103	9.1	1790	1	MMRP1	tenascin beta-1 cha
125	103	9.1	4753	1	A47437	LDL-receptor-relat
126	102.5	9.1	782	2	A61635	tenascin-like prot
127	102.5	9.1	1372	2	T25933	hypothetical prote
128	102.5	9.1	1746	1	A19694	tenascin precursor
129	102.5	9.1	4544	1	S02352	alpha-2-microglobu
130	101.5	9.1	3575	2	S14458	tenascin precursor
131	101.5	9.1	3575	2	S14458	tenascin precursor
132	101.5	9.1	3575	2	S14458	tenascin precursor
133	101.5	9.1	3575	2	S14458	tenascin precursor
134	100.5	9.0	1081	2	T31329	receptor tyrosine
135	100.5	9.0	2201	2	A21160	tenascin-C - human
136	100.5	9.0	4545	1	S25111	alpha-2-microglobu
137	100.5	9.0	1408	2	S16148	gene secreted prote
138	100.5	9.0	2019	1	J01322	tenascin precursor
139	100.5	9.0	3084	1	MMPSA	tenascin alpha-1 ch
140	100.5	9.0	1133	1	EGRT	epidermal growth f
141	100.5	9.0	1133	1	EGRT	epidermal growth f
142	100.5	9.0	1133	1	EGRT	epidermal growth f
143	100.5	9.0	1133	1	EGRT	epidermal growth f
144	100.5	9.0	1133	1	EGRT	epidermal growth f
145	100.5	9.0	1133	1	EGRT	epidermal growth f
146	100.5	9.0	1133	1	EGRT	epidermal growth f
147	100.5	9.0	1133	1	EGRT	epidermal growth f
148	100.5	9.0	1133	1	EGRT	epidermal growth f
149	100.5	9.0	1133	1	EGRT	epidermal growth f
150	100.5	9.0	1133	1	EGRT	epidermal growth f
151	100.5	9.0	1133	1	EGRT	epidermal growth f
152	100.5	9.0	1133	1	EGRT	epidermal growth f
153	100.5	9.0	1133	1	EGRT	epidermal growth f
154	100.5	9.0	1133	1	EGRT	epidermal growth f
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156	100.5	9.0	1133	1	EGRT	epidermal growth f
157	100.5	9.0	1133	1	EGRT	epidermal growth f
158	100.5	9.0	1133	1	EGRT	epidermal growth f
159	100.5	9.0	1133	1	EGRT	epidermal growth f
160	100.5	9.0	1133	1	EGRT	epidermal growth f
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162	100.5	9.0	1133	1	EGRT	epidermal growth f
163	100.5	9.0	1133	1	EGRT	epidermal growth f
164	100.5	9.0	1133	1	EGRT	epidermal growth f
165	100.5	9.0	1133	1	EGRT	epidermal growth f
166	100.5	9.0	1133	1	EGRT	epidermal growth f
167	100.5	9.0	1133	1	EGRT	epidermal growth f
168	100.5	9.0	1133	1	EGRT	epidermal growth f
169	100.5	9.0	1133	1	EGRT	epidermal growth f
170	100.5	9.0	1133	1	EGRT	epidermal growth f
171	100.5	9.0	1133	1	EGRT	epidermal growth f
172	100.5	9.0	1133	1	EGRT	epidermal growth f
173	100.5	9.0	1133	1	EGRT	epidermal growth f
174	100.5	9.0	1133	1	EGRT	epidermal growth f
175	100.5	9.0	1133	1	EGRT	epidermal growth f

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